



BLAST Basic Local Alignment Search Tool

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BLASTN programs search nucleotide subjects using a nucleotide query. [more...](#)

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Enter Query Sequence

Enter accession number, gi, or FASTA sequence [\[?\]](#) [Clear](#)

Query sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format or the input. To allow this feature there are certain conventions required with regard to the input of identifiers. [more...](#)

NM_022162

Query subrange [\[?\]](#)

From

To

Enter coordinates for a **subrange** of the query sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length. The range includes the residue at the **To** coordinate. [more...](#)

Or, upload file

 [\[?\]](#)

Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Genetic code

 ▼

Job Title

Enter a descriptive title for your BLAST search [\[?\]](#)

This title appears on all BLAST results and saved searches.

☒ Align two or more sequences [\[?\]](#)

To get the CDS annotation in the output, use only the NCBI accession or gi number for either the query or subject. Reformat the results and check 'CDS feature' to display that annotation.

Enter Subject Sequence

Enter accession number, gi, or FASTA sequence [\[?\]](#) [Clear](#)

Subject sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format or the input. To allow this feature there are certain conventions required with regard to the input of identifiers. [more...](#)

Subject subrange [\[?\]](#)From To

Enter coordinates for a **subrange** of the subject sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length. The range includes the residue at the **To** coordinate. [more...](#)

Or, upload file

[\[?\]](#)

Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Choose Search Set

Database

☒ Human genomic + transcript ☐ Mouse genomic + transcript ☐ Others (nr etc.):

Human genomic plus transcript (Human G+T) [\[?\]](#)

Select the sequence database to run searches against. No BLAST database contains all the sequences at NCBI. BLAST databases are organized by informational content (nr, RefSeq, etc.) or by sequencing technique (WGS, EST, etc.). [more...](#)

Organism

Optional

Enter organism name or id--completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [\[?\]](#)

Select from the list or choose "Custom" to enter the name of an organism. The search will be restricted to the sequences in the database which are from the organism selected.

Entrez Query

Optional

Enter an Entrez query to limit search [\[?\]](#)

You can use Entrez query syntax to search a subset of the selected BLAST database. This can be helpful to limit searches to molecule types, sequence lengths or to exclude organisms. [more...](#)

Program Selection

Optimize for

- ☐ Highly similar sequences (megablast)
☐ More dissimilar sequences (discontiguous megablast)
☒ Somewhat similar sequences (blastn)

Choose a BLAST algorithm [\[?\]](#)

- Megablast is intended for comparing a query to closely related sequences and works best if the target percent identity is 95% or more but is very fast.
- Discontiguous megablast uses an initial seed that ignores some bases (allowing mismatches) and is intended for cross-species comparisons.
- BlastN is slow, but allows a word-size down to seven bases.

[more...](#)

Algorithm

- ☐ blastp (protein-protein BLAST)
- ☐ PSI-BLAST (Position-Specific Iterated BLAST)
- ☐ PHI-BLAST (Pattern Hit Initiated BLAST)

Enter a PHI pattern [\[?\]](#)

Enter a PHI pattern to start the search. PHI-BLAST may perform better than simple pattern searching because it filters out false positives (pattern matches that are probably random and not indicative of homology).

Choose a BLAST algorithm [\[?\]](#)

- BlastP simply compares a protein query to a protein database.
- PSI-BLAST allows the user to build a PSSM (position-specific scoring matrix) using the results of the first BlastP run.)
- PHI-BLAST performs the search but limits alignments to those that match a pattern in the query.

BLAST

Search nucleotide sequence using Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

Algorithm parameters

General Parameters

Max target sequences

100 [\[?\]](#)

Select the maximum number of aligned sequences to display [\[?\]](#)

Maximum number of aligned sequences to display (the actual number of alignments may be greater than this).

Short queries

☒ Automatically adjust parameters for short input sequences [\[?\]](#)

Automatically adjust word size and other parameters to improve results for short queries.

Expect threshold

10 [\[?\]](#)

Expected number of chance matches in a random model. [more...](#)


Word size

11  [\(?\)](#)

The length of the seed that initiates an alignment. [more...](#)

Scoring Parameters

Matrix

PAM30  [\(?\)](#)

Assigns a score for aligning pairs of residues, and determines overall alignment score. [more...](#)

Match/Mismatch Scores

2,-3  [\(?\)](#)

Reward and penalty for matching and mismatching bases. [more...](#)

Gap Costs

Existence: 5 Extension: 2  [\(?\)](#)

Cost to create and extend a gap in an alignment. Linear costs are available only with megablast and are determined by the match/mismatch scores. [more...](#)

Compositional adjustments

No adjustment  [\(?\)](#)

Matrix adjustment method to compensate for amino acid composition of sequences. [more...](#)

Filters and Masking

Filter

☒ Low complexity regions [\(?\)](#)

Mask regions of low compositional complexity that may cause spurious or misleading results. [more...](#)

☐ Species-specific repeats for: Human  [\(?\)](#)

Mask repeat elements of the specified species that may lead to spurious or misleading results. [more...](#)

Mask

☒ Mask for lookup table only [\(?\)](#)

Mask query while producing seeds used to scan database, but not for extensions. [more...](#)

☐ Mask lower case letters [\[?\]](#)

Mask any letters that were lower-case in the FASTA input. [more...](#)

Discontiguous Word Options

Template length

18 [\[?\]](#)

Total number of bases in a seed that ignores some positions. [more...](#)

Template type

Coding [\[?\]](#)

Specifies which bases are ignored in scanning the database. [more...](#)

PSI/PHI BLAST

PSSM

PSSM is uploaded... [Clear](#)

Upload PSSM Optional

[Browse...](#) [\[?\]](#)

Upload a Position Specific Score Matrix (PSSM) that you previously downloaded from a PSI-BLAST iteration. You may search a different database than that used to generate the PSSM, but you must use the same query. [more...](#)

PSI-BLAST Threshold

[\[?\]](#)

Set the statistical significance threshold to include a sequence in the model used by PSI-BLAST to create the PSSM on the next iteration.

BLAST

Search nucleotide sequence using Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

7 [\[?\]](#) 28 [\[?\]](#) 11 [\[?\]](#) Linear [\[?\]](#) Linear [\[?\]](#) Linear [\[?\]](#) Linear [\[?\]](#)
 Linear [\[?\]](#) Existence: 5 Extension: 2 [\[?\]](#)

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BLAST Basic Local Alignment Search Tool



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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

gi|14277249|gb|AC007728.4|AC007728

Description

Homo sapiens chromosome 16 clone RP11-327F22, complete sequence

Molecule type

nucleic acid

Subject Length

168271

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string L;m;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

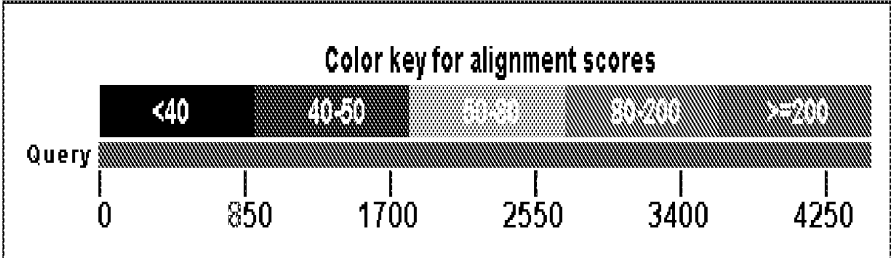
Effective search space 750722576

Graphic Summary

Distribution of 28 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.







Plot of gi|11545911|ref|NM_022162.1| vs gi|14277249|gb|AC007728.4|AC007728 [2]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions


Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

AC007728.4	Homo sapiens chromosome 16 clone RP11-327F22, complete sequence	3279	8591	100%	0.0	100%
------------	---	------	------	------	-----	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>**gb|AC007728.4|AC007728**  Homo sapiens chromosome 16 clone RP11-327F22, complete sequence
Length=168271

Sort alignments for this subject sequence by:
E value **Score** **Percent identity**
Query start position **Subject start position**

Score = 3279 bits (3636), Expect = 0.0
Identities = 1818/1818 (100%), Gaps = 0/1818 (0%)
Strand=Plus/Minus

Query	750	AGCTGCCACATGCAAGAAGTATATGGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCTCG	809
Sbjct	140450	AGCTGCCACATGCAAGAAGTATATGGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCTCG	140391
Query	810	CTTCCTCAGTACCTATGATGGAGCAGAGACGCTCTGCCTGGAGGACATATACACAGAGAA	869
Sbjct	140390	CTTCCTCAGTACCTATGATGGAGCAGAGACGCTCTGCCTGGAGGACATATACACAGAGAA	140331
Query	870	TGTCCTGGAGGCTGGGCAGATGTGGGCATGGCTGGACCCCGCAGAAGAGCCAGCCAC	929
Sbjct	140330	TGTCCTGGAGGCTGGGCAGATGTGGGCATGGCTGGACCCCGCAGAAGAGCCAGCCAC	140271
Query	930	CCTGGGCCTGGAGGAGCTCTTCAGCACCCCTGGCCACCTCAATGACGATGCGGACACTGT	989
Sbjct	140270	CCTGGGCCTGGAGGAGCTCTTCAGCACCCCTGGCCACCTCAATGACGATGCGGACACTGT	140211
Query	990	GCTGGTGGTGGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT	1049
Sbjct	140210	GCTGGTGGTGGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT	140151
Query	1050	GTGGGCTGCAGGGCAAGACTTCCAGGAATTTCTTTGTCTTCCATTTCAGTGCCGGCA	1109
Sbjct	140150	GTGGGCTGCAGGGCAAGACTTCCAGGAATTTCTTTGTCTTCCATTTCAGTGCCGGCA	140091
Query	1110	GCTGCAGTGCATGGCCAAACCACTCTCTGTGCGGACTCTACTCTTTGAGCACTGCTGTTG	1169
Sbjct	140090	GCTGCAGTGCATGGCCAAACCACTCTCTGTGCGGACTCTACTCTTTGAGCACTGCTGTTG	140031
Query	1170	GCCTGATGTTGGTCAAGAAGACATCTTCAGTTACTCCTTGACCACCCTGACCGTGTCT	1229
Sbjct	140030	GCCTGATGTTGGTCAAGAAGACATCTTCAGTTACTCCTTGACCACCCTGACCGTGTCT	139971

Query	1230	GTTAACCTTTGATGGCTTTGACGAGTTCAAGTTCAGGTTACGGATCGTGAACGCCACTG	1289
Sbjct	139970	GTTAACCTTTGATGGCTTTGACGAGTTCAAGTTCAGGTTACGGATCGTGAACGCCACTG	139911
Query	1290	CTCCCCGACCGACCCACCTCTGTCCAGACCCTGCTCTTCAACCTTCTGCAGGGCAACCT	1349
Sbjct	139910	CTCCCCGACCGACCCACCTCTGTCCAGACCCTGCTCTTCAACCTTCTGCAGGGCAACCT	139851
Query	1350	GCTGAAGAATGCCCCGAAGGTGGTGACCAGCCGTCCGGCCGCTGTGTCGGCGTTCTCAG	1409
Sbjct	139850	GCTGAAGAATGCCCCGAAGGTGGTGACCAGCCGTCCGGCCGCTGTGTCGGCGTTCTCAG	139791
Query	1410	GAAGTACATCCGCACCGAGTTCAACCTCAAGGGCTTCTCTGAACAGGGCATCGAGCTGTA	1469
Sbjct	139790	GAAGTACATCCGCACCGAGTTCAACCTCAAGGGCTTCTCTGAACAGGGCATCGAGCTGTA	139731
Query	1470	CCTGAGGAAGCGCCATCATGAGCCCGGGTGGCGGACCGCTCATCCGCCTGCTCCAAGA	1529
Sbjct	139730	CCTGAGGAAGCGCCATCATGAGCCCGGGTGGCGGACCGCTCATCCGCCTGCTCCAAGA	139671
Query	1530	GACCTCAGCCCTGCACGGTTTGTGCCACCTGCCTGTCTTCTCATGGATGGTGTCAAATG	1589
Sbjct	139670	GACCTCAGCCCTGCACGGTTTGTGCCACCTGCCTGTCTTCTCATGGATGGTGTCAAATG	139611
Query	1590	CCACCAGGAAGTGTGCTGCAGGAAGGGGGTCCCCAAAGACCACTACAGATATGTACCT	1649
Sbjct	139610	CCACCAGGAAGTGTGCTGCAGGAAGGGGGTCCCCAAAGACCACTACAGATATGTACCT	139551
Query	1650	GCTGATTCTGCAGCATTTTCTGCTGCATGCCAGGGGGAGACTCAGCTTCCCAAGGTCT	1709
Sbjct	139550	GCTGATTCTGCAGCATTTTCTGCTGCATGCCAGGGGGAGACTCAGCTTCCCAAGGTCT	139491
Query	1710	GGGACCCAGTCTTCTTCGGGGCCGCTCCCCACCCTCCTGCACCTGGGCAGACTGGCTCT	1769
Sbjct	139490	GGGACCCAGTCTTCTTCGGGGCCGCTCCCCACCCTCCTGCACCTGGGCAGACTGGCTCT	139431
Query	1770	GTGGGGCTGGGCATGTGCTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT	1829
Sbjct	139430	GTGGGGCTGGGCATGTGCTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT	139371
Query	1830	CAGCCCTGATGACATTTCTTGGCTTCCTGGTGCGTGCCAAAGGTGTCGTGCCAGGGAG	1889
Sbjct	139370	CAGCCCTGATGACATTTCTTGGCTTCCTGGTGCGTGCCAAAGGTGTCGTGCCAGGGAG	139311
Query	1890	TACGGCGCCCCTGGAATTCCTTCACATCACTTTCCAGTGCTTCTTGCCGCGTTCTACCT	1949
Sbjct	139310	TACGGCGCCCCTGGAATTCCTTCACATCACTTTCCAGTGCTTCTTGCCGCGTTCTACCT	139251
Query	1950	GGCACTCAGTGCTGATGTGCCACCAGCTTTGCTCAGACACCTCTTCAATTGTGGCAGGCC	2009
Sbjct	139250	GGCACTCAGTGCTGATGTGCCACCAGCTTTGCTCAGACACCTCTTCAATTGTGGCAGGCC	139191
Query	2010	AGGCAACTCACCAATGGCCAGGCTCCTGCCCACGATGTGCATCCAGGCTCGGAGGGAAA	2069
Sbjct	139190	AGGCAACTCACCAATGGCCAGGCTCCTGCCCACGATGTGCATCCAGGCTCGGAGGGAAA	139131
Query	2070	GGACAGCAGCGTGGCAGCTTTGCTGCAGAAGGCCGAGCCGACAACTTCAGATCACAGC	2129
Sbjct	139130	GGACAGCAGCGTGGCAGCTTTGCTGCAGAAGGCCGAGCCGACAACTTCAGATCACAGC	139071
Query	2130	AGCCTTCCTGGCAGGGCTGTTGTCCCGGAGCACTGGGGCTGCTGGCTGAGTGCCAGAC	2189

```
Sbjct 139070 AGCCTTCCTGGCAGGGCTGTTGTCCCGGAGCACTGGGGCTGCTGGCTGAGTGCCAGAC 139011
Query 2190 ATCTGAGAAGGCCCTGCTCCGGCGCCAGGCCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT 2249
          |||
Sbjct 139010 ATCTGAGAAGGCCCTGCTCCGGCGCCAGGCCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT 138951
Query 2250 CCGCAAGCACTTCCACTCCATCCCGCCAGCTGCACCGGGTGAGGCCAAGAGCGTGTCATGC 2309
          |||
Sbjct 138950 CCGCAAGCACTTCCACTCCATCCCGCCAGCTGCACCGGGTGAGGCCAAGAGCGTGTCATGC 138891
Query 2310 CATGCCCCGGGTTTCATCTGGCTCATCCGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC 2369
          |||
Sbjct 138890 CATGCCCCGGGTTTCATCTGGCTCATCCGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC 138831
Query 2370 TCGGAAGGCTGCACGTGGCCTGAATGTTGGGCACCTCAAGTTGACATTTGCAGTGTGGG 2429
          |||
Sbjct 138830 TCGGAAGGCTGCACGTGGCCTGAATGTTGGGCACCTCAAGTTGACATTTGCAGTGTGGG 138771
Query 2430 CCCCCTGAGTGTGCTGCCCTGGCCTTTGTGCTGCAGCACCTCCGGCGGCCCGTGGCCCT 2489
          |||
Sbjct 138770 CCCCCTGAGTGTGCTGCCCTGGCCTTTGTGCTGCAGCACCTCCGGCGGCCCGTGGCCCT 138711
Query 2490 GCAGCTGGACTACAACCTCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTTGCCTTGG 2549
          |||
Sbjct 138710 GCAGCTGGACTACAACCTCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTTGCCTTGG 138651
Query 2550 TGTCTGCAAGGCTCTGTA 2567
          |||
Sbjct 138650 TGTCTGCAAGGCTCTGTA 138633
```

Score = 2401 bits (2662), Expect = 0.0
Identities = 1331/1331 (100%), Gaps = 0/1331 (0%)
Strand=Plus/Minus

```
Query 3155 GGCTCCGAGGGAACACTTTCTCTCTAGAGGAGGTTGACAAGCTCGGCTGCAGGGACACCA 3214
          |||
Sbjct 119260 GGCTCCGAGGGAACACTTTCTCTCTAGAGGAGGTTGACAAGCTCGGCTGCAGGGACACCA 119201
Query 3215 GACTCTTGCTTTGAAGTCTCCGGGAGGATGTTCTGCTCAGTTTGTGTTGTGAGCAGGCTGT 3274
          |||
Sbjct 119200 GACTCTTGCTTTGAAGTCTCCGGGAGGATGTTCTGCTCAGTTTGTGTTGTGAGCAGGCTGT 119141
Query 3275 GAGTTTGGGCCCCAGAGGCTGGGTGACATGTGTTGGCAGCCTCTTCAAAATGAGCCCTGT 3334
          |||
Sbjct 119140 GAGTTTGGGCCCCAGAGGCTGGGTGACATGTGTTGGCAGCCTCTTCAAAATGAGCCCTGT 119081
Query 3335 CCTGCCTAAGGCTGAACCTGTTTTCTGGGAACACCATAGGTACCTTTATTCTGGCAGAG 3394
          |||
Sbjct 119080 CCTGCCTAAGGCTGAACCTGTTTTCTGGGAACACCATAGGTACCTTTATTCTGGCAGAG 119021
Query 3395 GAGGGAGCATCAGTGCCCTCCAGGATAGACTTTTCCCAAGCCTACTTTTGCCATTGACTT 3454
          |||
Sbjct 119020 GAGGGAGCATCAGTGCCCTCCAGGATAGACTTTTCCCAAGCCTACTTTTGCCATTGACTT 118961
Query 3455 CTTCCTAAGATTCAATCCAGGATGTACAAGGACAGCCCTCCTCCATAGTATGGGACTG 3514
          |||
Sbjct 118960 CTTCCTAAGATTCAATCCAGGATGTACAAGGACAGCCCTCCTCCATAGTATGGGACTG 118901
Query 3515 GCCTCTGCTGATCCTCCAGGCTTCCGTGTGGGTGAGTGGGGCCCATGGATGTGCTTGTT 3574
          |||
Sbjct 118900 GCCTCTGCTGATCCTCCAGGCTTCCGTGTGGGTGAGTGGGGCCCATGGATGTGCTTGTT 118841
```

```
Query 3575 AACTGAGTGCCTTTTGGTGGAGAGGCCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC 3634
|||||
Sbjct 118840 AACTGAGTGCCTTTTGGTGGAGAGGCCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC 118781

Query 3635 TGATGAAGAGGAGTACACAGAACACATAATTAGGAAGCAGCTTTCCCATGTCTCGACT 3694
|||||
Sbjct 118780 TGATGAAGAGGAGTACACAGAACACATAATTAGGAAGCAGCTTTCCCATGTCTCGACT 118721

Query 3695 CATCCATCCAGGCCATTCCCGTCTCTGGTTCTCCCTCCTCCTGGACTCCTGCACACG 3754
|||||
Sbjct 118720 CATCCATCCAGGCCATTCCCGTCTCTGGTTCTCCCTCCTCCTGGACTCCTGCACACG 118661

Query 3755 CTCCTTCCTCTGAGGCTGAAATTCAGAATATTAGTGACCTCAGCTTTGATATTTCACTTA 3814
|||||
Sbjct 118660 CTCCTTCCTCTGAGGCTGAAATTCAGAATATTAGTGACCTCAGCTTTGATATTTCACTTA 118601

Query 3815 CAGCACCCCCAACCTGGCACCCAGGGTGGGAAGGGCTACACCTTAGCCTGCCCTCCTTT 3874
|||||
Sbjct 118600 CAGCACCCCCAACCTGGCACCCAGGGTGGGAAGGGCTACACCTTAGCCTGCCCTCCTTT 118541

Query 3875 CCGGTGTTTAAGACATTTTGAAGGGGACACGTGACAGCCGTTTGTCCCCAAGACATT 3934
|||||
Sbjct 118540 CCGGTGTTTAAGACATTTTGAAGGGGACACGTGACAGCCGTTTGTCCCCAAGACATT 118481

Query 3935 CTAGGTTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTTATTT 3994
|||||
Sbjct 118480 CTAGGTTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTTATTT 118421

Query 3995 CCAGTGAAATCAGTTACTCTTCAGTTAAGCCTTTGGAACAGCTCGACTTTAAAAAGCTC 4054
|||||
Sbjct 118420 CCAGTGAAATCAGTTACTCTTCAGTTAAGCCTTTGGAACAGCTCGACTTTAAAAAGCTC 118361

Query 4055 CAAATGCAGCTTTAAAAAATTAATCTGGGCCAGAATTTCAAACGGCCTCACTAGGCTTCT 4114
|||||
Sbjct 118360 CAAATGCAGCTTTAAAAAATTAATCTGGGCCAGAATTTCAAACGGCCTCACTAGGCTTCT 118301

Query 4115 GGTGATGCCTGTGAAGTGAAGTCTGACAAACAGACTTCTGAAATAGACCCACAAGAGGCA 4174
|||||
Sbjct 118300 GGTGATGCCTGTGAAGTGAAGTCTGACAAACAGACTTCTGAAATAGACCCACAAGAGGCA 118241

Query 4175 GTTCCATTTCAATTTGTGCCAGAATGCTTTAGGATGTACAGTTATGGATTGAAAGTTTACA 4234
|||||
Sbjct 118240 GTTCCATTTCAATTTGTGCCAGAATGCTTTAGGATGTACAGTTATGGATTGAAAGTTTACA 118181

Query 4235 GGaaaaaaaATTAGGCCGTTTCCTTCAAAGCAAATGTCTTCTGGATTATTCAAATGATG 4294
|||||
Sbjct 118180 GGAAAAAAAAATTAGGCCGTTTCCTTCAAAGCAAATGTCTTCTGGATTATTCAAATGATG 118121

Query 4295 TATGTTGAAGCCTTTGTAAATTGTCAGATGCTGTGCAAATGTTATTATTTTAAACATTAT 4354
|||||
Sbjct 118120 TATGTTGAAGCCTTTGTAAATTGTCAGATGCTGTGCAAATGTTATTATTTTAAACATTAT 118061

Query 4355 GATGTGTGAAACTGGTTAATATTTATAGGTCACCTTTGTTTTACTGTCTTAAGTTTATAC 4414
|||||
Sbjct 118060 GATGTGTGAAACTGGTTAATATTTATAGGTCACCTTTGTTTTACTGTCTTAAGTTTATAC 118001

Query 4415 TCTTATAGACAACATGGCCGTGAACCTTATGCTGTAAATAATCAGAGGGGAATAAACTGT 4474
|||||
Sbjct 118000 TCTTATAGACAACATGGCCGTGAACCTTATGCTGTAAATAATCAGAGGGGAATAAACTGT 117941

Query 4475 TGAGTCAAAAC 4485
|||||
Sbjct 117940 TGAGTCAAAAC 117930
```

Score = 848 bits (940), Expect = 0.0
Identities = 473/475 (99%), Gaps = 0/475 (0%)
Strand=Plus/Minus

```
Query 172      TCTCCGGGTTGTGAAATGTGCTCGCAGGAGGCTTTTCAGGCACAGAGGAGCCAGCTGGTC 231
               || || |||||
Sbjct 151525   TCCCCAGGTTGTGAAATGTGCTCGCAGGAGGCTTTTCAGGCACAGAGGAGCCAGCTGGTC 151466

Query 232      GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCGAGAGTGTCTGGACTGGCTGCTGTCC 291
               |||||
Sbjct 151465   GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCGAGAGTGTCTGGACTGGCTGCTGTCC 151406

Query 292      TGGGAGGTCCTCTCCTGGGAGGACTACGAGGGCTTCCACCTCCTGGGCCAGCCTCTCTCC 351
               |||||
Sbjct 151405   TGGGAGGTCCTCTCCTGGGAGGACTACGAGGGCTTCCACCTCCTGGGCCAGCCTCTCTCC 151346

Query 352      CACTTGGCCAGGCGCCTTCTGGACACCGTCTGGAATAAGGGTACTTGGGCCTGTGAGAAG 411
               |||||
Sbjct 151345   CACTTGGCCAGGCGCCTTCTGGACACCGTCTGGAATAAGGGTACTTGGGCCTGTGAGAAG 151286

Query 412      CTCATCGCGGCTGCCAAGAAGCCCAGGCCGACAGCCAGTCCCCCAAGCTGCATGGCTGC 471
               |||||
Sbjct 151285   CTCATCGCGGCTGCCAAGAAGCCCAGGCCGACAGCCAGTCCCCCAAGCTGCATGGCTGC 151226

Query 472      TGGGACCCCCACTCGCTCCACCCAGCCCAGACCTGCAGAGTCACCGCCAGCCATTGTC 531
               |||||
Sbjct 151225   TGGGACCCCCACTCGCTCCACCCAGCCCAGACCTGCAGAGTCACCGCCAGCCATTGTC 151166

Query 532      AGGAGGCTCCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGGAGCGGGGTTTCGTC 591
               |||||
Sbjct 151165   AGGAGGCTCCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGGAGCGGGGTTTCGTC 151106

Query 592      AGCCAGTATGAATGTGATGAAATCAGGTTGCCGATCTTCACACCGTCCCAGAGGG 646
               |||||
Sbjct 151105   AGCCAGTATGAATGTGATGAAATCAGGTTGCCGATCTTCACACCGTCCCAGAGGG 151051
```

Score = 325 bits (360), Expect = 6e-90
Identities = 180/180 (100%), Gaps = 0/180 (0%)
Strand=Plus/Minus

```
Query 1        GTAGACAGATCCAGGCTCACCAGTCTGTGCCACTGGGCTTTTGGCGTTCTGCACAAGGC 60
               |||||
Sbjct 153867   GTAGACAGATCCAGGCTCACCAGTCTGTGCCACTGGGCTTTTGGCGTTCTGCACAAGGC 153808

Query 61       CTACCCGAGATGCCAIGCCTGTCTCCCCAGCCTAATGGGCTTTGATGGGGGAAGAGGGT 120
               |||||
Sbjct 153807   CTACCCGAGATGCCAIGCCTGTCTCCCCAGCCTAATGGGCTTTGATGGGGGAAGAGGGT 153748

Query 121      GGTTACGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCTCCTCGGACATTCTCCGGGT 180
               |||||
Sbjct 153747   GGTTACGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCTCCTCGGACATTCTCCGGGT 153688
```

Score = 194 bits (214), Expect = 3e-50
Identities = 107/107 (100%), Gaps = 0/107 (0%)
Strand=Plus/Minus

```
Query 645      GGCAAGAAGGCTGCTTGATCTTGCCACGGTGAAAGCGAATGGATTGGCTGCCTTCCTTCT 704
               |||||
Sbjct 143152   GGCAAGAAGGCTGCTTGATCTTGCCACGGTGAAAGCGAATGGATTGGCTGCCTTCCTTCT 143093
```

Query 705 ACAACATGTTTCAGGAATTACCAGTCCCATTTGGCCCTGCCTTTGGAAG 751
|||||
Sbjct 143092 ACAACATGTTTCAGGAATTACCAGTCCCATTTGGCCCTGCCTTTGGAAG 143046

Score = 158 bits (174), Expect = 2e-39
Identities = 87/87 (100%), Gaps = 0/87 (0%)
Strand=Plus/Minus

Query 2987 GCCTGGAGGAGAACCATCTCCAGGATGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA 3046
|||||
Sbjct 125518 GCCTGGAGGAGAACCATCTCCAGGATGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA 125459

Query 3047 AAAATTCAAGTTTGAAAATCCTGAAGT 3073
|||||
Sbjct 125458 AAAATTCAAGTTTGAAAATCCTGAAGT 125432

Score = 158 bits (174), Expect = 2e-39
Identities = 87/87 (100%), Gaps = 0/87 (0%)
Strand=Plus/Minus

Query 2901 CAGCCTGGTGGGGAACAACATTGGCAGTGTGGGTGCCCAAGCCTTGGCACTGATGCTGGC 2960
|||||
Sbjct 127708 CAGCCTGGTGGGGAACAACATTGGCAGTGTGGGTGCCCAAGCCTTGGCACTGATGCTGGC 127649

Query 2961 AAAGAACGTCATGCTAGAAGAACTCTG 2987
|||||
Sbjct 127648 AAAGAACGTCATGCTAGAAGAACTCTG 127622

Score = 156 bits (172), Expect = 6e-39
Identities = 86/86 (100%), Gaps = 0/86 (0%)
Strand=Plus/Minus

Query 2734 AGGCTGGGGAATAACTACATCACTGCCGCGGGAGCCCAAGTGTGCGCGAGGGGCTCCGA 2793
|||||
Sbjct 131083 AGGCTGGGGAATAACTACATCACTGCCGCGGGAGCCCAAGTGTGCGCGAGGGGCTCCGA 131024

Query 2794 GGCAACACCTCCTTGCACTTCTGGG 2819
|||||
Sbjct 131023 GGCAACACCTCCTTGCACTTCTGGG 130998

Score = 154 bits (170), Expect = 2e-38
Identities = 85/85 (100%), Gaps = 0/85 (0%)
Strand=Plus/Minus

Query 3072 GTTGTCCAATAACTGCATCACCTACCTAGGGGCAGAAGCCCTCCTGCAGGCCCTTGAAAG 3131
|||||
Sbjct 121188 GTTGTCCAATAACTGCATCACCTACCTAGGGGCAGAAGCCCTCCTGCAGGCCCTTGAAAG 121129

Query 3132 GAATGACACCATCCTGGAAGTCTGG 3156
|||||
Sbjct 121128 GAATGACACCATCCTGGAAGTCTGG 121104

Score = 154 bits (170), Expect = 2e-38
Identities = 85/85 (100%), Gaps = 0/85 (0%)
Strand=Plus/Minus

Query 2819 GATTCTGGGGCAACAGAGTGGGTGACGAGGGGGCCAGGCCCTGGCTGAAGCCTTGGGTG 2878


```
|||||
Sbjct  128385  GATTCTGGGGCAACAGAGTGGGTGACGAGGGGGCCAGGCCCTGGCTGAAGCCTTGGGTG 128326
Query  2879    ATCACCAGAGCTTGAGGTGGCTCAG 2903
|||||
Sbjct  128325  ATCACCAGAGCTTGAGGTGGCTCAG 128301
```

Score = 154 bits (170), Expect = 2e-38
Identities = 85/85 (100%), Gaps = 0/85 (0%)
Strand=Plus/Minus

```
Query  2652    TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG 2711
|||||
Sbjct  134115  TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG 134056
Query  2712    CAGGCAGAACTTCTTGGCATTGAGG 2736
|||||
Sbjct  134055  CAGGCAGAACTTCTTGGCATTGAGG 134031
```

Score = 154 bits (170), Expect = 2e-38
Identities = 90/92 (97%), Gaps = 1/92 (1%)
Strand=Plus/Minus

```
Query  2561    CTCGTGA-TTTGCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT 2619
|||| || |||||
Sbjct  134427  CTCITTAGTTTTCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT 134368
Query  2620    GCTCTTCACTGCGAGCAATTGCAGAAGTTAGC 2651
|||||
Sbjct  134367  GCTCTTCACTGCGAGCAATTGCAGAAGTTAGC 134336
```

Score = 35.6 bits (38), Expect = 0.015
Identities = 22/24 (91%), Gaps = 0/24 (0%)
Strand=Plus/Plus

```
Query  4221    ATTGAAAGTTTACAGGaaaaaaaa 4244
||| | |||||
Sbjct  60530    ATTAACAGTTTACAGGAAAAAAAA 60553
```

Score = 30.1 bits (32), Expect = 0.63
Identities = 18/19 (94%), Gaps = 0/19 (0%)
Strand=Plus/Plus

```
Query  281     GGCTGCTGTCCTGGGAGGT 299
||| |||||
Sbjct  131339  GGCAGCTGTCCTGGGAGGT 131357
```

Score = 30.1 bits (32), Expect = 0.63
Identities = 18/19 (94%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query  339     CCAGCCTCTCTCCCACTTG 357
|| |||||
Sbjct  136285  CCTGCCTCTCTCCCACTTG 136267
```

Score = 30.1 bits (32), Expect = 0.63
Identities = 16/16 (100%), Gaps = 0/16 (0%)

Strand=Plus/Plus

```
Query  1098      CAGCTGCCGGCAGCTG  1113
          |||||
Sbjct  140087    CAGCTGCCGGCAGCTG  140102
```

Score = 28.3 bits (30), Expect = 2.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

```
Query  2801      CCTCCTTGCAGTTCC  2815
          |||||
Sbjct  8417      CCTCCTTGCAGTTCC  8403
```

Score = 28.3 bits (30), Expect = 2.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

```
Query  953       GCACCCCTGGCCACC  967
          |||||
Sbjct  109718    GCACCCCTGGCCACC  109732
```

Score = 28.3 bits (30), Expect = 2.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus

```
Query  2283      ACCGGGTGAGGCCAAGAGCGTGCAT  2307
          || || |||| |||||
Sbjct  160465    ACAGGCTGAGTGCAAGAGCGTGCAT  160489
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

```
Query  1064      AAGACTTCCAGGAA  1077
          |||||
Sbjct  1485      AAGACTTCCAGGAA  1472
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 26/34 (76%), Gaps = 0/34 (0%)
Strand=Plus/Minus

```
Query  1608      GCAGGAggggggTCCCCAAAGACCACTACAGAT  1641
          ||||| |||| || |||||
Sbjct  10423    GCAGGAGGTCCTGTCCCTCAAACCACTACAGAT  10390
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  3051      TTCAAGTTTGAAAA  3064
          |||||
Sbjct  68988     TTCAAGTTTGAAAA  69001
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)

Strand=Plus/Plus

```
Query  4154  GAAATAGACCCACA  4167
          |||||
Sbjct  79121  GAAATAGACCCACA  79134
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  3807  TTCACCTACAGCAC  3820
          |||||
Sbjct  120449 TTCACCTACAGCAC  120462
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

```
Query  2983  CTCTGCCTGGAGGA  2996
          |||||
Sbjct  140359 CTCTGCCTGGAGGA  140346
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

```
Query  3015  AGGTGTA GTTCTC  3028
          |||||
Sbjct  143043 AGGTGTA GTTCTC  143030
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 17/19 (89%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query  4060  GCAGCTTTAAAAAATTAAT  4078
          ||| |||||
Sbjct  160764 GCATCTTTAAAAAATAAAT  160746
```

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  3015  AGGTGTA GTTCTC  3028
          |||||
Sbjct  164997 AGGTGTA GTTCTC  165010
```

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